

T400X SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Lok, Si  
Adams, Robyn L.  
Jelberg, Anna C.  
Whitmore, Theodore E.  
Farrah, Theresa M.

(ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: ZymoGenetics  
(B) STREET: 1201 Eastlake Ave East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Lunn, Paul G  
(B) REGISTRATION NUMBER: 32,743

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(C) REFERENCE/DOCKET NUMBER: 97-52

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6627
- (B) TELEFAX: 206-442-6678
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 34...1755

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC	54		
Met Arg Thr Leu Leu Thr Ile			
1	5		
TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT	102		
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp			
10	15	20	
CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG	150		
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu			
25	30	35	
ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC	198		
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile			
40	45	50	55
GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT	246		
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys			
60	65	70	

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CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC			294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn			
75	80	85	
CTC ACG GAG CTC TAC TAT GCC AGG GTC ACC GCT GTC AGT GCG GGA GGC			342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly			
90	95	100	
CGG TCA GCC ACC AAG ATG ACT GAC AGG TTC AGC TCT CTG CAG CAC ACT			390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr			
105	110	115	
ACC CTC AAG CCA CCT GAT GTG ACC TGT ATC TCC AAA GTG AGA TCG ATT			438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile			
120	125	130	135
CAG ATG ATT GTT CAT CCT ACC CCC ACG CCA ATC CGT GCA GGC GAT GGC			486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly			
140	145	150	
CAC CGG CTA ACC CTG GAA GAC ATC TTC CAT GAC CTG TTC TAC CAC TTA			534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu			
155	160	165	
GAG CTC CAG GTC AAC CGC ACC TAC CAA ATG CAC CTT GGA GGG AAG CAG			582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln			
170	175	180	
AGA GAA TAT GAG TTC TTC GGC CTG ACC CCT GAC ACA GAG TTC CTT GGC			630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly			
185	190	195	
ACC ATC ATG ATT TGC GTT CCC ACC TGG GCC AAG GAG AGT GCC CCC TAC			678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr			
200	205	210	215
ATG TGC CGA GTG AAG ACA CTG CCA GAC CGG ACA TGG ACC TAC TCC TTC			726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe			
220	225	230	
TCC GGA GCC TTC CTG TTC TCC ATG GGC TTC CTC GTC GCA GTA CTC TGC			774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys			
235	240	245	

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TAC CTG AGC TAC AGA TAT GTC ACC AAG CCG CCT GCA CCT CCC AAC TCC Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser 250	255	260	822
CTG AAC GTC CAG CGA GTC CTG ACT TTC CAG CCG CTG CGC TTC ATC CAG Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln 265	270	275	870
GAG CAC GTC CTG ATC CCT GTC TTT GAC CTC AGC GGC CCC AGC AGT CTG Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu 280	285	290	295
GCC CAG CCT GTC CAG TAC TCC CAG ATC AGG GTG TCT GGA CCC AGG GAG Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu 300	305	310	966
CCC GCA GGA GCT CCA CAG CGG CAT AGC CTG TCC GAG ATC ACC TAC TTA Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu 315	320	325	1014
GGG CAG CCA GAC ATC TCC ATC CTC CAG CCC TCC AAC GTG CCA CCT CCC Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro 330	335	340	1062
CAG ATC CTC TCC CCA CTG TCC TAT GCC CCA AAC GCT GCC CCT GAG GTC Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val 345	350	355	1110
GGG CCC CCA TCC TAT GCA CCT CAG GTG ACC CCC GAA GCT CAA TTC CCA Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro 360	365	370	375
TTC TAC GCC CCA CAG GCC ATC TCT AAG GTC CAG CCT TCC TCC TAT GCC Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala 380	385	390	1206
CCT CAA GCC ACT CCG GAC AGC TGG CCT CCC TCC TAT GGG GTA TGC ATG Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met 395	400	405	1254
GAA GGT TCT GGC AAA GAC TCC CCC ACT GGG ACA CTT TCT AGT CCT AAA Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys 410	415	420	1302

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CAC CTT AGG CCT AAA GGT CAG CTT CAG AAA GAG CCA CCA GCT GGA AGC 1350  
 His Leu Arg Pro Lys Gly Glu Leu Glu Lys Glu Pro Pro Ala Gly Ser  
 425 430 435

TGC ATG TTA GGT GGC CTT TCT CTG CAG GAG GTG ACC TCC TTG GCT ATG 1398  
 Cys Met Leu Gly Gly Leu Ser Leu Glu Val Thr Ser Leu Ala Met  
 440 445 450 455

GAG GAA TCC CAA GAA GCA AAA TCA TTG CAC CAG CCC CTG GGG ATT TGC 1446  
 Glu Glu Ser Glu Ala Lys Ser Leu His Glu Pro Leu Gly Ile Cys  
 460 465 470

ACA GAC AGA ACA TCT GAC CCA AAT GTG CTA CAC AGT GGG GAG GAA GGG 1494  
 Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly  
 475 480 485

ACA CCA CAG TAC CTA AAG GGC CAG CTC CCC CTC CTC TCC TCA GTC CAG 1542  
 Thr Pro Glu Tyr Leu Lys Glu Glu Leu Pro Leu Leu Ser Ser Val Glu  
 490 495 500

ATC GAG GGC CAC CCC ATG TCC CTC CCT TTG CAA CCT CCT TCC GGT CCA 1590  
 Ile Glu Gly His Pro Met Ser Leu Pro Leu Glu Pro Pro Ser Gly Pro  
 505 510 515

TGT TCC CCC TCG GAC CAA GGT CCA AGT CCC TGG GGC CTG CTG GAG TCC 1638  
 Cys Ser Pro Ser Asp Glu Glu Pro Ser Pro Trp Glu Leu Leu Glu Ser  
 520 525 530 535

CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA 1686  
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser  
 540 545 550

GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC 1734  
 Asp Leu Glu Glu Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala  
 555 560 565

CTG ACT GTG CAG TGG GAG TCC TGAGGGAAAT GGGAAAGGCT TGGTGCTTCC TCCC 1789  
 Leu Thr Val Glu Trp Glu Ser  
 570

TGTCCCTACC CAGTGTACCA TCCTTGGCTG TCAATCCCAT GCCTGCCAT GCCACACACT 1849  
 CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGGC ATGCAGGGCC 1909  
 CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCAGGGGA 1969  
 GCTCTGGGGA GCAGCTTG TGAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT 2029  
 GACAGTGCAA GGAGGAAATG CAGGGAAACT CCCGAGGTCC AGAGCCCCAC CTCCTAACAC 2089

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CATGGATTCA	AAGTGCTCAG	GGAATTGCC	TCTCCTTGC	CCATTCTGG	CCAGTTCAC	2149
AATCTAGCTC	GACAGAGCAT	GAGGCCCTG	CCTCTTCTGT	CATTGTTCAA	AGGTGGGAAG	2209
AGAGCCTGGA	AAAGAACAG	GCCTGGAAA	GAACCAGAAG	GAGGCTGGC	AGAACCCAGAA	2269
CAACCTGCAC	TTCTGCCAAG	GCCAGGGCCA	GCAGGACGGC	AGGACTCTAG	GGAGGGGTGT	2329
GGCCTGCAGC	TCATTCCCAG	CCAGGGCAAC	TGCCTGACGT	TGCACGATT	CAGCTTCATT	2389
CCTCTGATAG	AACAAAGCGA	AATGCAGGTC	CACCAGGGAG	GGAGACACAC	AAGCCTTTTC	2449
TGCAGGCAGG	AGTTTCAGAC	CCTATCTGA	GAATGGGGTT	TGAAAGGAAG	GTGAGGGCTG	2509
TGGCCCCTGG	ACGGGTACAA	TAACACACTG	TACTGATGTC	ACAACCTTGC	AAGCTCTGCC	2569
TTGGGTTTCAG	CCCATCTGGG	CTCAAATTCC	AGCCTCACCA	CTCACAAGCT	GTGTGACTTC	2629
AAACAAATGA	AATCAGTGCC	CAGAACCTCG	GTTCCTCAT	CTGTAATGTG	GGGATCATAA	2689
CACCTACCTC	ATGGAGTTGT	GGTGAAGATG	AAATGAAGTC	ATGTCTTAA	AGTGCTTAAT	2749
AGTGCCTGGT	ACATGGGCAG	TGCCAATAA	ACGGTAGCTA	TTTAAAAAAA	AAAAAAAAAA	2809
AAAAAAATAG	CGGCCGCCTC	GA				2831

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His	
1			5					10						15		
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	
								20			25			30		
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	
								35			40			45		
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	
								50			55			60		
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	
								65			70			75		80
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	
								85			90			95		
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	
								100			105			110		
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	
								115			120			125		
Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	
								130			135			140		

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Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
 145 150 155 160  
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
 165 170 175  
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
 180 185 190  
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
 195 200 205  
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp  
 210 215 220  
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly  
 225 230 235 240  
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys  
 245 250 255  
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe  
 260 265 270  
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp  
 275 280 285  
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile  
 290 295 300  
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser  
 305 310 315 320  
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln  
 325 330 335  
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala  
 340 345 350  
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val  
 355 360 365  
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys  
 370 375 380  
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro  
 385 390 395 400  
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr  
 405 410 415  
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
 420 425 430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
 435 440 445  
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
 450 455 460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465 470 475 480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu  
 485 490 495

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Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
 500 505 510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
 515 520 525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
 530 535 540  
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp  
 545 550 555 560  
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser  
 565 570

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAACTTGA AAACATCCTG ACGTGGGACA CGGGGCCAGA GGGCACCCCA GACACGGTCT	60
ACAGCATCGA GTATAANACG TACGGAGAGA GGGACTGGGT GGCAAAGAAAN GGCTGTCAGC	120
GGATCACCCG GAAGTCCTGC AACCTGACGG TGGAGACGGG CAACCTCACG GAGCTCTACT	180
ATGCCAGGGT CACCGCTGTC AGTGCAGGGAG GCCGGTCANC CACCAAGATG ACTGACAGGT	240
TCAGCTCTCT GCAGCACACT ACCCTCAAGC CACCTGATGT GACCTGTATC TCCAAAGTGA	300
GATCGATTCTN GATGATTGTT CATCCTACCC CCACGCCAAT CCGTGCAGGC GATG	354

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AACATCCTGA CGTGGGACAG CGGGCCAGAG	30
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## (2) INFORMATION FOR SEQ ID NO:5:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTISENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGTCACA TCAGGTGGCT TGAGGGTAGT

30

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCTGGGTTC GCTACTCGAG GC GGCCGCTA TTTTTTTTTT TTTTTTTT

48

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